

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: March 14, 2003, 02:07:45 ; Search time 2645.71 Seconds

(without alignments)
1579.326 Million cell updates/sec

Title: US-09-698-781-3
Perfect score: 1436
Sequence: 1 MKOILHPALLETMTLPVL.....KHOLYRDSKASCNCNSIY 258

Scoring table:
BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 16154066 segs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL-frame+ p2n.model -DEV-xlh
-O/cgn2_1/USPRO.spool/US09698781/runat_07032003_083459_5329/app.query.fasta.1.654
-DB-EST -QFMT-fastap -SUFFIX-p2n.rst -MINMATCH-0.1 -LOOPEXT-0 -LOOPEXT-0
-UNITS-bits -START-1 -END-1 -MATRIX-Biosum62 -TRANS-human40.cdi -LIST-45
-DOCALLIGN-200 -THR SCORE-pct -THR MAX-100 -THR MIN-0 -ALIGN-15 -MODE-LOCAL
-OUTFMT-pio -NORM-ext -HEAPSIZE-500 -MINLEN-0 -MAXLEN-200000000
-USER-US09698781.cgn.1.1.2463 -runat_07032003_083459_5329 -NCPU-6 -ICPU-3
-NO_XLPRY -NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -LONGLOG -DEV.TIMEOUT-120
-MARK.TIMEOUT-30 -THRAD-1 -XGAPOP-10 -XGAPEXT-0.5 -Fgapop-6 -Fgapext-7
-YGAPOP-10 -YGAPEXT-0.5 -DELOP-6 -DELEXT-7

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estio:*
8: em_htc:*
9: gb_estcl:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vit:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_pod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	965	67.2	547	9 AL703262	AL703262 DKF2P686K
2	943	65.7	1037	13 BM554122	BM554122 ACBNCOURT
3	943	65.7	1108	13 BM52843	BM52843 ACBNCOURT
4	912	63.5	1063	13 BM559790	BM559790 ACBNCOURT
5	869	60.5	803	13 BM826346	BM826346 603076094
6	867	60.4	450	12 BF897404	BF897404 IL2-MT018
7	867	60.4	808	13 BM826697	BM826697 603077463
8	858	59.7	462	12 BF897377	BF897377 IL2-MT018
9	858	59.7	781	13 BM829771	BM829771 603079842
10	850	59.2	464	12 BF897410	BF897410 IL2-MT018
11	830	57.8	451	12 BF897412	BF897412 IL2-MT018
12	825	57.5	443	12 BF897401	BF897401 IL2-MT018
13	823.5	57.3	904	13 BM830749	BM830749 603075145
14	814	56.7	420	12 BF897378	BF897378 IL2-MT018
15	814	56.7	784	13 BM825564	BM825564 603072524
16	807.5	56.2	946	12 BF832357	BF832357 603072889
17	796	55.4	454	12 BF897368	BF897368 IL2-MT018
18	782.5	54.5	728	13 BM827352	BM827352 603077880
19	780	54.3	806	13 BM826010	BM826010 603076409
20	772.5	53.8	1414	11 AK009449	AK009449 Mus muscu
21	769	53.6	406	12 BF897379	BF897379 IL2-MT018
22	762	53.1	952	12 BG721420	BG721420 602694975
23	761.5	53.0	784	13 BM829333	BM829333 603071465
24	761.5	53.0	864	13 BM460544	BM460544 603201164
25	758	52.8	760	12 BG722432	BG722432 602693657
26	748	52.1	801	13 BM831850	BM831850 603078978
27	741	51.6	764	13 BM829788	BM829788 603079859
28	740	51.5	722	12 BG723701	BG723701 602697894
29	739	51.5	742	13 BM460734	BM460734 603204913
30	737	51.3	730	13 BM559392	BM559392 603253072
31	736	51.3	721	13 BM830127	BM830127 603072754
32	729	50.8	769	13 BM825992	BM825992 603076580
33	719.5	50.1	865	12 BG721972	BG721972 602696722
34	710.5	49.5	708	13 BM156058	BM156058 603254682
35	707	49.2	740	12 BG724382	BG724382 602692860
36	706.5	49.2	821	12 BG722866	BG722866 602695346
37	706	49.2	401	12 BF897366	BF897366 IL2-MT018
38	696	48.5	852	12 BM553721	BM553721 603190658
39	695.5	48.4	843	12 BG723588	BG723588 602694310
40	692.5	48.2	705	13 BM683698	BM683698 603306249
41	689.5	48.0	769	13 BM464694	BM464694 603202325
42	679.5	47.3	849	13 BM562149	BM562149 603255338
43	673.5	46.9	600	10 BE588308	BE588308 196937 BA
44	671.5	46.8	674	13 BM691604	BM691604 603307276
45	670	46.7	870	13 BM465248	BM465248 603204748

ALIGNMENTS

RESULT 1
AL703262
LOCUS AL703262 547 bp mRNA linear EST 22-MAR-2002
DEFINITION DKF2P686K1819.r1 686 (synonym: h1cc3) Homo sapiens cDNA clone
AL703262
ACCESSION AL703262
VERSION AL703262.1 GI:19686617
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 547)
AUTHORS Poustka,A., Wellenreuther,R., Mewes,H.W., Well,B. and Wiemann,S.).
TITLE EST (Poustka,A., Wellenreuther,R., Mewes,H.W., Well,B. and Wiemann

JOURNAL
COMMENT

,S.)
Unpublished (1999)
Contact: Poustka A.J.
Department Lehrach
Max-Planck-Institute for Molecular Genetics
Inhestasse 73, 14195 Berlin, Germany
Tel: +49-30-84131623
Fax: +49-30-84131128
Email: poustka@mpg-berlin-dahlem.mpg.de
This is the 5' sequence of the clone insert
Cloned from S. Mleemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ), Email: s.wiemann@dkfz-heidelberg.de;
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project.
No sl sequence available.
This clone (DKFZ686K1819) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers

FEATURES

source
1..547
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKFZ686K1819"
/clone_1lb="686 (synonym: hicc3)"
/tissue_type="human skeletal muscle"
/dev_stage="adult"
/lab_host="DH10B"
/note="Vector: pT7-1pLX2; site_1: Sflra; site_2: Sflib;
cDNA-collection"

BASE COUNT 170 a 120 c 120 g 137 t
ORIGIN

Alignment Scores:

Pred. No.: 5,98e-99 Length: 547
Score: 965.00 Matches: 179
Percent Similarity: 98.908 Conservatve: 0
Best Local Similarity: 98.908 Mismatches: 2
Query Match: 67.208 Indels: 0
DB: 9 Gaps: 0

US-09-698-781-3 (1-258) x AL703262 (1-547)

QY 1 MetLysGlnIleLeuHisProAlaLeuGluThrAlaMetThrLeuPheProValLeu 20
DB 4 ATGAACAACAAATCTCATCTCTCGAACCACACGCAATGACATTTATCCAGTCTG 63
QY 21 LeuPheLeuValAlaGlyLeuLeuProSerPheProAlaAsnGluAspLysAspProAla 40
DB 64 TTGTTCTGCTGGTGGCTGCTCCATCTTTCCAGCAAAATGAAGATAGGATCCGCT 123
QY 41 PheThrAlaLeuLeuThrThrgInThrGlnValGlnArgGluIleValAsnLysHisAsn 60
DB 124 TTTACTGCTTTTAAACCCCAACACAGTCAAGGACATGTTGATTAAGCAAT 183
QY 61 GluLeuArgArgAlaValSerProProAlaArgAsnMetLeuLysMetCyluThrPasnLys 80
DB 184 GAACGAGAGAGACGATATCTCCCTGCCAACAACATCTGAAGATGGAATGGAACAA 243
QY 81 GluAlaAlaAlaAsnAlaGlnLysTrpAlaAsnGlnCysAsnTrpArgHisSerAsnPro 100
DB 244 GAGGCTGCAGCAAAATGCCCAAAAGTGGCAACCACTGCAATTAACGACAGTAACCA 303
QY 101 LysAspArgMetThrSerLeuLysCysGlyLysAsnLeuLysMetSerSerAlaProSer 120
DB 304 AAGGATCGAATGACAACTTAATATGCTGCAATCTTACATGTCGAAGTGCCTCAGC 363
QY 121 SerTPSPSerGlnAlaIleGlnSerTrpPheAspGluTrpAsnAspPheAspPheGlyVal 140
DB 364 TCATGGTCAACAGCAATCCAAAGCTGGTTGATGATACAAATGATTTTACCTTGGTGA 423
QY 141 GlyProLysThrProAsnAlaValAlaGlyHisTrpThrGlnValValTrpTyrSerSer 160

DB 424 GGGCCAAAGCTCCCAACGACGCTGTGGACATTTATACACAGCTTGTGTACTCTTCA 483
QY 161 TyrLeuValGlyCysGlyAsnAlaTrpCysProAsnGlnLysValLeuLysTrpTyr 180
DB 484 TACCTCGGTGATGTGGAAATGCCACTCTCCCATCAAAAAGTCTTAATAATCACTAT 543

QY 181 Val 181
DB 544 GTT 546

RESULT 2
BMS54122
LOCUS BMS54122 1037 bp mRNA linear EST 20-FEB-2002
DEFINITION AGENCOURT_6546919 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5742354
5', mRNA sequence.
ACCESSION BMS54122
VERSION BMS54122.1 GI:18793449
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1037)
AUTHORS NIH-MGC http://mhc.ncl.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM12760 row: f column: 19
High quality sequence stop: 385.
Location/Qualifiers

FEATURES

source
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5742354"
/clone_1lb="NIH_MGC_119"
/tissue_type="medulla"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: EcoRV (destroyed); RNA source normal medulla from
anonymous male age 27. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.3 kb. Insert size range
0.9-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 013. Note:
this is a NIH-MGC Library."

BASE COUNT 318 a 223 c 228 g 266 t 2 others
ORIGIN

Alignment Scores:

Pred. No.: 5,27e-96 Length: 1037
Score: 943.00 Matches: 177
Percent Similarity: 78.63% Conservatve: 29
Best Local Similarity: 67.56% Mismatches: 50
Query Match: 65.67% Indels: 6
DB: 13 Gaps: 3

US-09-698-781-3 (1-258) x BMS54122 (1-1037)

QY 1 MetLysGlnIleLeuHisProAlaLeuGluThrThr-----AlaMetThrLeuPhePr 18
DB 153 ATAAAGTAGATATTTCATCTCTCGAAGAAACACATTTCCAGCATGCTTTACTACC 212
QY 18 oValLeuLeuPheLeuValAlaGlyLeuLeuProSerPheProAlaAsnGluAspLysAs 38

Db 213 GGGG---TTGTTCTGTTACTGTGCTGCTCCATCTTACTGCA---GAAGGAAGA 266
 Oy 38 pRoAlaPheThrAlaLeuLeuThrThGlnThrGlnValGlnArgGluLeuAlaAsn 58
 Db 267 TCCCCCTTTTACTGCTTTGTTTAACCAAGGAGTGTGCAAGGAGGAGATTTGAATTA 326
 Oy 58 sHIsAnGluLeuArgAlaValSerProProAlaArgAsnMetLeuLeuMetGluTr 78
 Db 327 ACACATGAAGTAAAGCAAGAGTCTCTCCACCTGCCAATAACATGCTAAAGATGGAATG 386
 Oy 78 pAsnLySGluAlaAlaAlaAsnAlaGlnLyStrpAlaAsnGlnCysAsnTyArgHisSe 98
 Db 387 GAGCAGAGAGGTAACAGCAATGCCCCAAGGGGGAACCAAGTGCACCTTACACATAG 446
 Oy 98 rAsnProLyAspArgMetThrSerLeuLeuScylGluAsnLeuTyMetSerSerAl 118
 Db 447 TGATCCAGAGGAGCCGCAAAACAGTACAGATGTGTGAGAACTCTATATGTCAAGTGA 506
 Oy 118 aProSerSerTPSerGlnAlaIleGlnSerTrpPheAspGluTyArgAsnPhAsp 138
 Db 507 CCTACTTCTCTGCTCTCTGCAATCCAAAGCTGTGATGAGAGATCCCTAGATTGTCTA 566
 Oy 138 eGlyValGlyProLyStrpProAsnAlaValAlaGlyHisTyThrGlnValValTrpTy 158
 Db 567 TGGTGTAGACCAAGAGATGCCAATGCACTGTGTGACATTTACTACACTGTGTGTA 626
 Oy 158 rSerSerTyLeuValGlyCysGlyAsnAlaTyrcysProAsnGlnValLeuLysTy 178
 Db 627 CTCGACTTCCAGGAGCGGTGTGGAATGCTCTACTGCTCCCAATCAAGATAGTCAAAAA 686
 Oy 178 rTyTyValCysGlnTyrcysProAlaGlyAsnTrpAlaAsnArgLeuTyValProTy 198
 Db 687 CTACTATGTTTCCATATGTTCTGCTGCTGNTATATGATGAAAGAAATACCCGTA 746
 Oy 198 rGluGlnGly-AlaProCysAlaSerCysProAspAsnGlyLeuCysThra 218
 Db 747 CCACACAGGAACACCTGTGCGGTGCGGTGATGACGTGGAACAAGCATATGACACA 806
 Oy 218 srGlyCysAlaTyrcyluAspLeuTyrcysAsnGlySerLeuLeuThrThc 238
 Db 807 AATAGTCCAGATCAAGATCTCTCAAGTACTGATTCCTTGAAGAAATACAGCTGCT 866
 Oy 238 yLysHisGlnLeuValArgAspSerCysAlaSerCysAsnGlySerSerAsnSerIleT 258
 Db 867 GTGACATAGATTACTCAAGGAAGGCAAGGCTACTTGCCTATGTGACAGCAAAATT 926
 Oy 258 yr 258
 Db 927 AC 928
 RESULT 3
 LOCUS BM552843 1108 bp mRNA linear EST 20-FEB-2002
 DEFINITION AGENCOURT_6542520 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5742685
 5', mRNA sequence.
 ACCESSION BM552843
 VERSION BM552843.1 GI:18791053
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE 1 (bases 1 to 1108)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:
 http://image.lnl.gov
 Plate: LLM12761 row: d column: 14
 High quality sequence stop: 700.
 Location/Qualifiers
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5742685"
 /clone_id="NIH_MGC_119"
 /tissue_type="medulla"
 /lab_host="DH10B"
 /note="Organ: brain; Vector: pCMV-SPORT6; Site:1: NotI;
 Site:2: EcoRV (destroyed); RNA source normal medulla from
 anonymous male age 27. Library is oligo-dT primed and
 directionally cloned (EcoRV site is destroyed upon
 cloning). Average insert size 1.3 kb. Insert size range
 0.9-3 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 013. Note:
 this is a NIH_MGC Library."
 BASE COUNT 341 a 236 c 235 g 291 t 5 others
 ORIGIN
 Alignment Scores:
 Pred. No.: 5 87e-96 Length: 1108
 Score: 943.00 Matches: 172
 Percent Similarity: 82.57% Conservative: 27
 Best Local Similarity: 71.37% Mismatches: 40
 Query Match: 65.67% Indels: 3
 DB: 13 Gaps: 2
 US-09-698-781-3 (1-258) x BM552843 (1-1108)
 Oy 13 AlaMetThrLeuPheProValLeuLeuPheLeuValAlaGlyLeuLeuProSerPhePro 32
 Db 136 GCATGGCTTACTACTACGGTG---TTGTTCTGTTACTGCTGCTGCTCATCTTACT 192
 Oy 33 AlaAsnGluAspLysAspProAlaPheThrAlaLeuLeuThrThrGlnValGln 52
 Db 193 GCA---GAAGGAAGATCCCGCTTTACTGCTTTTAAACCAAGTGTGCAAGTGA 249
 Oy 53 ArgGluIleValAsnLysHisAsnGluLeuArgArgAlaValSerProProAlaAsn 72
 Db 250 AGGAGATTTGTAATTAACACATGAACATGAAGCAAGCACTCTCCACTGCAATAC 309
 Oy 73 MetLeuLysMetGluTrpAsnLysGluAlaAlaAlaAsnAlaGlnLyStrpAlaAsnGln 92
 Db 310 ATGCTAAGATGGAATGAGAGAGAGAGAGATCAACCAATGCCCAAGGCTGGCAACAG 369
 Oy 93 CysAsnTyArgHisSerAsnProLyAspArgMetThrSerLeuLysCylGluAsn 112
 Db 370 TGACCTTACACATATGTGTGTCAGAGAGCCGCAAAACGATCAAGATGTGTGCAAT 429
 Oy 113 LeuTyMetSerSerAlaProSerSerTrpSerGlnAlaIleGlnSerTrpPheAspGlu 132
 Db 430 CTTATATGTCAGATGACCTACTCTCTGCTCTTGCACATCCAAAGCTGTGATGAGAG 489
 Oy 133 TyrAsnAspPheAspPheGlyValGlyProLyStrpProAsnAlaValAlaGlyHisTy 152
 Db 490 ATCTAGATTGTTGTCATGTGTGAGACCAAGAGTCCCAATCCAGTTGTGACATTTAT 549
 Oy 153 ThrGlnValValTrpTySerSerTyrcysAlaGlyCysGlnAlaTyrcysProAsn 172
 Db 550 ACTCAGCTGTGTGACTGCTTACCCAGGTGAGTGTGCAATGCTGCTGTAATATGAAAT 609
 Oy 173 GlnLyValLeuLysTyrcyluAspLeuTyrcysProAlaGlyAsnTrpAlaAsn 192
 Db 610 CAGATAGCTTAATAACTACTATGTTGCCAATATGCTCTGCTGTAATATGAAAT 669
 Oy 193 ArgLeuTyValProTyrcyluGlnGlyAlaProCysAlaSerCysProAspAsn 212
 Db 670 AGAAGATACCCGCTACCAAGCAAGCAACCTGTGCGGTGCTGCTGCTGATGCTGAC 729

OY	213	AspG1LleucCysThrAsnGlyCysLysTYRGLAspLeuTYrSerAsnCysLysSerLeu	232
Db	730	MAAGGACTATGCACCAATAGTGTCCAGTATCAAGATCTCTAAGTACTGTGATTCCTTG	789
OY	233	LysLeuThrLeuThrCysLysSHisGlnLeuValArgAspSerCysLysAsaSerCysAsn	252
Db	790	AAGTACACAGCTGC-CGTGTAACATGAGTACTACACAGAAACAGACAGGCTACTTCCCTA	848
OY	253	Cys 253	
Db	849	TGT 851	
RESULT 4			
LOCUS	BM559790	1063 bp	mRNA linear EST 20-FEB-2002
DEFINITION	AGENCOURT_6565524 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5744414		
ACCESSION	BM559790		
VERSION	BM559790.1	GI:18803670	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	1 (bases 1 to 1063)		
JOURNAL	NIH-MGC http://mhc.ncl.nih.gov/ .		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue procurement: Life Technologies, Inc. cDNA library preparation: Life Technologies, Inc. cDNA library arrayed by: The I.M.A.G.E. Consortium (LNL) DNA sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov Plate: LLM12765 row: 1 column: 15 High quality sequence stop: 618. Location/Qualifiers 1. 1063 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_image="5744414" /clone_lib="NIH_MGC_119" /tissue_type="medulla" /lab_host="DH10B" /note="Organ: brain; Vector: pCMV-SPORT6; site:1; Note: site:2; EcoRV (destroyed): RNA source normal medulla from anonymous male age 27. Library is oligo-dt primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NIH MGC Library." BASE COUNT 317 a 235 c 240 g 271 t ORIGIN		
Alignment Scores:			
Pred. No.:	1.79e-92	Length:	1063
Score:	912.00	Matches:	170
Percent Similarity:	80.42%	Conservative:	23
Best Local Similarity:	70.83%	Mismatches:	44
Query Match:	63.51%	Indels:	4
DB:	13	Gaps:	2
US-09-698-781-3 (1-258) x BM559790 (1-1063)			
OY	13	AlaMetThrLeuPheProValLeuLeuPheLeuValAlaGlyLeuLeuProSerSerPhePro	32
Db	172	GCAATGCTTACTACTACCGGTG--TTGTTTGTGTGCTGTGCTTCATCTTACTACT	228

FEATURES	LOCATION/QUALIFIERS
QY	33 AlaAsnGlnAspSerProAlaPheThrAlaLeuLeuThrThrcGlnGlnValGln 52
Db	229 GCA---GAAAGAAAGCATCCCTCTTTACTGCTTTGTATACCAACCCAGTTGCAAGGCA 285
QY	53 ArgGluIleValAsnLysHisAsnGlnIleLeuArgArgAlaValSerProProAlaArgAsn 72
Db	286 AGGAGATGTGTAATTAACGACATGAACTAAGAAGACGTCCTCCACTCCAGTAAC 345
QY	73 MetLeuLysMetClnUtrpAsnLysGlnAlaAlaAlaAsnAlaGlnLysTrpAlaAsnGln 92
Db	346 ATGCTAAACATGGAAGGAGGACAGAGAGCTACCAACCAATGCCCAAGCTGGCCAAACAAAG 405
QY	93 CysAsnTrpArgHisSerAsnProLysAspArgMetThrSerLeuLysCysGlnLysAsn 112
Db	406 TGCACCTTTCACACATGATGTATCCAGGAGACCCGAAACCAAGTACAGATGTGTAGAT 465
QY	113 LeuTrpMetSerSerAlaProSerSerTrpSerGlnAlaIleGlnSerTrpPheAspGlu 132
Db	466 CTCATATGTCGAAGTACACCTACTCTCTGTCTTCTGCATATCCAAAGCTGGTATACGAG 525
QY	133 TyrAsnAspPheAspPheGlyValGlyProLysTrpProAsnAlaValAlaGlyHisIstyr 152
Db	526 ATCCTAGATTTGTCTATGCTGTAGACCAAGACCAAGATCCCAATGCAAGTGTTCGACATTAT 585
QY	153 ThrGlnValValTrpTrpSerSerTrpLeuValGlyCysGlyAsnAlaIstyrCysProAsn 172
Db	586 ACTCACTGTGTGTGGTACTGACCTTACCAAGTACGTTGGTGAATTTGCTTACTGCTCCAT 645
QY	173 GlnLysValLeuLysIstyrTrpValCysGlnTrpCysProAlaGlyAsnTrpAlaAsn 192
Db	646 CAAGATAGCTAAATATACATATGTTCCCAATATTTGCTGCTGGTATATATATGAT 705
QY	193 ArgLeuTrpValProTyrGlnGlnGlyAlaProCysAlaSerCysProAspAsnCysAsp 212
Db	706 ACAAAGAAATACCCCGTACCCCAAGAACACCTTTGGCCGGGTGCTGATGACTGAC 765
QY	213 AspGlyLeuCysThrAsnGlyCysLysTrpGluAspLeuTrpSerAsnCysLysSerLe 232
Db	766 AAGAGCTATGCAACCAATAGTTGCCAGTATCAAGATCTCCCTAAGACATGGGAACTCTT 825
QY	232 uLysLeuThrIleuThrCysLysHisGlnLeuValArgAspSerCysLysAlaSerCys 251
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RESULT 5	
BI826346	
LOCUS	BI826346
DEFINITION	603076094F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5168015 5',
ACCESSION	BI826346
VERSION	BI826346.1 GI:15937896
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
TITLE	NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgaabs-remail.nih.gov Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov Plate: LAM1417 row: k column: 24 High quality sequence stop: 799. Location/Qualifiers

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/tissue_type="medulla"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMV-Sport6; Site_1: NotI;
Site_2: EcoRV (destroyed); RNA source normal medulla from
anonymous male age 27. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.3 kb, insert size range
0.9-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(invitrogen). Research Genetics tracking code 013. Note:
this is a NIH_MGC Library."

BASE COUNT      250 a      183 c      166 g      204 t
ORIGIN

Alignment Scores:
Pred. No.:      8.45e-88      Length:      803
Score:          869.00      Matches:      160
Percent Similarity: 80.62%      Conservative: 23
Best Local Similarity: 70.48%      Mismatches: 41
Query Match:      60.52%      Indels:      3
DB:              13      Gaps:      2

US-09-698-781-3 (1-258) x B1826346 (1-803)
Oy 1 MettysGlnIleLeuHISProAlaLeuGlnIuThr---AlaMetThrLeuPheProVal 19
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Db 127 ATAAAGTAGATATTTCATCTCTCCAGAAACCAATTTCCAGCAATGGCTTTACTACC 186
Oy 20 LeuLeuPheLeuValaGlyLeuLeuProSerPheProAlaAsnGlnLysAspPro 39
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 187 GGTGCTTTCTGCTACTGCTGCTCTCCATCTTTACTGCA---GAAAGAAAGATCCC 243
Oy 40 AlaPheThrAlaLeuLeuThrThrGlnThrGlnValGlnArgGlnIleValAsnLysHis 59
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 244 GCTTTTACTGCTTTGTTAACCCAGCCAGTGCAGAGTCCAAAGGAGATTGTAATTAACAC 303
Oy 60 AsnGlnLeuArgArgAlaValSerProProAlaArgAsnMetLeuLysMetGlnIuPasn 79
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Oy 80 LysGlnAlaAlaAlaAsnAlaGlnLysTrpAlaAsnGlnCysAsnTyraArgHisSerAsn 99
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Db 364 AAGAGAGTAAACAAGCAATCCCAAGAGTGGGCAAAACAGTGCATTACACATAGTAGAT 423
Oy 100 ProLysAspArgMetThrSerLeuLysCysGlyGlnAsnLeuTyMetSerSerAlaPro 119
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Db 424 CCAAGAGACCCGAAACCAAGTACAGATGTGGTGAATCTCTATATGTCAAGTGAACCT 483
Oy 120 SerSerTrpSerGlnAlaIleGlnSerTrpPheAspGluTyraAsnSphAspPheGly 139
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Db 484 ACTTCTGCTGCTCTCCATTCACCAAGCTGATGACGAGATCTCATATTGTCATAGT 543
Oy 140 ValGlyProLysThrProAsnAlaValAla-GlyHisTyThrGlnValAlaTrpTyrse 159
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 544 GTAGGACCAAGAGTCCCATGCTGTTGGACATTTACTACACCTGTTGGTACTC 603
Oy 159 rSerTyrLeuValGlyCysGlyAsnAlaTyrcysProAsnGlnLysValLeuLysTyTy 179
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Db 604 GACTTACCAAGTAGGCTGTGGAAATTCCTACTGTCCTCCCAATCAAGATAGCTTAATAACTA 663
Oy 179 rTyValLysGlnIuTyCysProAlaGlyAsnTrpAlaAsnArgLeuTyValProTyrGln 199
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
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Oy 199 uGlnGlyAlaProCysAlaSerCysProAsnAsnCysAspAspGlyLeuLysThrAsnGln 219
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Oy 219 yCysLysTyrglnAspLeu 225
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Db 784 TTGCCAGTATCAAGATCTC 802

RESULT 6
BF897404
LOCUS
DEFINITION
BF897404
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 450)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Britones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.G.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the RPRESF/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?rl=1l2&t2=1l2-MT0181-
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High quality sequence stop: 449.

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Location/Qualifiers
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SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

BASE COUNT      138 a      94 c      96 g      122 t
ORIGIN

Alignment Scores:
Pred. No.:      5.55e-88      Length:      450
Score:          867.00      Matches:      148
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Best Local Similarity: 99.33%      Mismatches: 0
Query Match:      60.38%      Indels:      0
DB:              12      Gaps:      0

US-09-698-781-3 (1-258) x BF897404 (1-450)
Oy 87 GlnLysTrpAlaAsnGlnCysAsnTyraArgHisSerAsnProLysAspArgMetThrSer 106
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Oy 107 LeuLysCysGlyGlnAsnLeuTyMetSerSerAlaProSerSerTrpSerGlnAlaIle 126
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 QY 78 PASNLySGIULaAlaAlaAsnAlaGlnLysTrpAlaAsnGlnCysAsnTrpArgHisSe 98
 Db 362 GAGCAGAGAGGTAAACAAACAGATGCGCAAGAGTGGGCAACAGTCCACTTTACAACATAG 421
 QY 98 RASNPProLysAspArgMetThrSerLeuLysCysGlyLysAsnLeuTyrMetSerSerAl 118
 Db 422 TGATCCAGAGGACCCCAAAACAGTACAGATGTGTGAGAACTCTATATCTCAAGTGA 481
 QY 118 AProSerSerTrpSerGlnAlaAlaGlnSerTrpPheAspGluTyrAsnAspPheAspPh 138
 Db 482 CCTACTCTCTGCTGCTCTGCAATCCAAAGCTGATGACGAGATCCTAGATTGTGCTGA 541
 QY 138 eGlyValGlyProLysThrProAsnAlaValAlaGlyHisTrpTrpGlnValValTrpTy 158
 Db 542 TGGTGTAGGACCAAGAGTCCCAATGCAATGCTGTGACATTAATCTCAGCTGTGGTA 601
 QY 158 rSerSerTrpLeuValGlyCysGlyAsnAlaTyrCysProAsnGlnLysValLeuLysTy 178
 Db 602 CTCGACTTACCAAGTACAGCTGTGCAATGCTCTCTCCCAATCAAGATAGCTTAAATA 661
 QY 178 rTyTrpValCysGlnTrpCysProAlaGlyAsnTrpAlaAsnArgLeuTyrValProTy 198
 Db 662 CTACTATTTTGGCCAAATTTGCTGCTGCTGATATATATGATGAAGAATATACCCCGTA 721
 QY 198 rGluGlnGlyAlaProCysAlaSerCysProAspAsnCysAspAspGlyLeuCysThr 217
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 LOCUS IL2-MT0181-281100-265-604 MT0181 Homo sapiens cDNA, mRNA sequence.
 DEFINITION BF897410
 ACCESSION BF897410.1 GI:12288856
 VERSION EST.
 KEYWORDS human.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 464)
 AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Britones,M.R.,
 Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
 Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
 M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
 Simpson,A.J.
 TITLE Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/ICR Human Cancer Genome
 project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?el=IL2&ct=IL2-MT0181-
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 /note="Organ: marrow; Vector: puc18; Site1: Sma1; Site2:
 Sma1; A mini-library was made by cloning products derived
 from ORESTES PCR (U.S. Letters Patent application No. 196
 716 - Ludwig Institute for Cancer Research) profiles
 into the puc 18 vector. Reverse transcription of tissue
 mRNA and cDNA amplification were performed under low
 stringency conditions."

BASE COUNT 144 a 96 c 98 g 123 t 3 others
 ORIGIN

Alignment Scores:
 Pred. No.: 4,93e-86 Length: 464
 Score: 850.00 Matches: 149
 Percent Similarity: 96.77% Conservative: 1
 Best Local Similarity: 96.13% Mismatches: 4
 Query Match: 59.19% Indels: 1
 DB: 12 Gaps: 0

US-09-698-781-3 (1-258) x BF897410 (1-464)

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 QY 143 LysThrProAsnAlaValAlaGlyHisTrpTrpGlnValValTrpTySerSerTyLeu 162
 Db 162 AAGACTCCCAACTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 241
 QY 163 ValGlyCysGlyAsnAlaTyrCysProAsnGlnLysValLeuLysTyTrpTyValCys 182
 Db 242 GTTGATGTGGAATGGCGCTAGCTGCCAATCAAAAGTCTAAATACATATGTTGCG 301
 QY 183 GlnTrpCysProAlaGlyAsnTrpAlaAsnArgLeuTyrValProTyGluGlnGlyAla 202
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 QY 203 ProCysAlaSerCysProAspAsnCysAspAspGlyLeuCysThrAsnGlnCysLysTy 222
 Db 362 CTTGTGCGAGTGTGCCAGATACGTGTGCGATGCGATGCGATGCGATGCGATGCGATGCG 421
 QY 223 GluAspLeuTyrSerAsnCys-LysSerLeuLysLeuThrLeu 236
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 LOCUS IL2-MT0181-281100-265-610 MT0181 Homo sapiens cDNA, mRNA sequence.
 DEFINITION BF897412
 ACCESSION BF897412
 VERSION BF897412.1 GI:12288858
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 451)
 AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Britones,M.R.,
 Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
 Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
 M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
 Simpson,A.J.


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DB 322 CAGGTGTTGGTACTCTTCATACCTCGTGGAGAAATCCCTACTGTCCTCAATCA 263
QY 174 LysValLeuLysTyrTyrTyrValCysGlnTyrCysProAlaGlyAsnTyrPalaAsnArg 193
DB 262 AAGGTTCTAAATACCTACTACTGTTGTCCTCAATATGTCCTGCTGTAATGGCTTAATGA 203
QY 194 LeuTyrValProTyrGlnGlnGlyAlaProCysAlaSerCysProAspAsnCysAspAsp 213
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QY 214 GlyLeuCysThrAsnGlyCysLysTyrGluAspLeuTyrSerAsnCysLysSerLeuLys 233
DB 142 GACCTATGACCAATGCTGCAAGTACGAGATCTCTATAGTAACTGTAAGTTTGAAG 83
QY 234 LeuThrLeuThrCysLysHisGlnLeuValArgAspSerCysLysAlaSerCysAsnCys 253
DB 82 CTCACATTAACTGTAACATCAGTTGTCAGAGGACAGTTGCAAGACATCTCTCATTTGT 23
QY 254 SerAsnSerTyrTyr 258
DB 22 TCAACACGATTTAT 8
RESULT 13
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DEFINITION 603075145F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5167186 5',
ACCESSION B1830749
VERSION B1830749.1 GI:15942299
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 904)
NIH-MGC http://mhc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bcrfemail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM11415 row: 1 column: 11
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Site_2: EcoRV (destroyed); RNA source normal medulla from
anonymous male age 27. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.3 kb. Insert size range
0.9-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(invitrogen). Research Genetics tracking code 013. Note:
this is a NIH_MGC Library."
BASE COUNT 278 a 201 c 193 g 232 t
ORIGIN

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Score: 823.50 Matches: 170
Percent Similarity: 75.95% Conservative: 29
Best Local Similarity: 64.89% Mismatches: 50
Query Match: 57.35% Indels: 14
DB: 13 Gaps: 5
US-09-698-781-3 (1-258) x B1830749 (1-904)
QY 1 MetLysGlnIleLeuHisProAlaLeuGluThr-Thr-----AlaMetThrLeuPhePr 18
DB 125 ATAAATAGATATTTATCTCTGCTGAGAAACCAATTTCCAGCAATGCTTACTAC 184
QY 18 oValLeuLeuPheLeuValAlaGlyLeuLeuProSerPheProAlaAsnGluAspLysAs 38
DB 185 GGTG---TTGTTCTGCTACTGCTGCTGCTCATCTTACCTGCA---GAAGAAAGGA 238
QY 38 pProAlaPheThrAlaLeuLeuThrThrGlnThrGlnValGlnArgGluIleValAsnLys 58
DB 239 TCCCGCTTTACTGCTTTGTTAAACCCCAAGTTGCAAGTGCAAGGAGCAATTTGTAATA 298
QY 58 sHisAsnGluLeuValArgAlaValSerProProAlaArgAsnMetLeuLysMetGluTr 78
DB 299 ACACATGAACTAGAGAAAGAGCTCTCCACCTGCCAGTAACATCTAAAGTGAATG 358
QY 78 pAsnLysGluAlaAlaAlaAsnAlaGlnLysTyrPalaAsnGlnCysAsnTyrArgHisSe 98
DB 359 GACACAGAGAGTAAACACAGCATGCCCAAGGTGGCAACAGTGACCTTACACATAG 418
QY 98 rAsnProLysAspArgMetThrSerLeuLysCysGlyGluAsnLeuTyrMetSerSerL 118
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QY 118 aProSerSerTyrPserGlnAlaAlaIleGlnSerTyrPheAspGluTyrAsnAspPheAsp 138
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QY 138 eGlyValGlyProLysThrProAsnAlaValAlaGlyHisTyrThrGlnValValTrrPty 158
DB 538 TGGTGTAGAGACCAAAAGTCCCAATGACGTGTGACATTAATCACTGCTGTTGCTA 597
QY 158 rSerSerTyrLeuValGlyCysGlyAsnAlaTyrCysProAsnGlnLysValLeuLysTy 178
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RESULT 14
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DEFINITION IL2-MT0181-281100-265-A06 MT0181 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF897378
VERSION BF897378.1 GI:12288837
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 420)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,

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Alignment Scores:

1.47e-82 Length:

904


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Db 370 TGGAGCAGAGAGGTAAACACCAATGCCAAAGTGGCCAAACAGTGCACCTTTACACACT 429
QY 98 SerAsnProLysAspArgMetThrSerLeuLysCysGluAsnLeuTyrMetSerSer 117
Db 430 AGTGATCCAGAGAGCCGAAACAGTACAGATGCTGGAGAACTCTATATGTCAAGT 489
QY 118 AlaProSerSerTyrPheGlnAlaIleGlnSerTyrPheAspGluTyrAsnAspPheAsp 137
Db 490 GACCTACTCTCTGCTCTTCTGCAATCCAAAGCTGGTATGACGAGATCCTAGATTTCGTC 549
QY 138 PheGlyValGlyProLysThrProAsnAlaValValGlyHisTyrThrGlnValValTyrP 157
Db 550 TATGCTAGAGACCAAGAGTCCCAATGCAGTGTGGACATTTACTCAGCTGTGTTGG 609
QY 158 TyrSerSerTyrLeuValGlyCysGlyAsnAlaTyrCysProAsnGlnLysValLeuLys 177
Db 610 TACTCGACTTACCAAGTAGGCTGTGCAATGCTGCTACTGCTCCCAATCAAGATAGTCTAAA 669
QY 178 TyrTyrTyrValCysGlnTyrCysProAlaGlnTyrPalaAsnArgLeuTyrValPro 197
Db 670 TACTACTATGTGTTGCCAATATGTGCTGCTGTAATATATGCAATAGAAAGAAATACCCCG 729
QY 198 TyrGlnGlnGlyAlaProCysAla-SerCysProAsnAsnCysAspAspGlyLeu 215
Db 730 TACCACACAGGAAACCTTGTGCGGTTGCCCTGATGACTGTGCAAAAGGACTA 784
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Job time : 2648.71 secs